

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Sutcliffe, Gregor J., et al.)
Division of) Prior Art Unit: 1653
Serial No.: 09/230,896)
Filed: December 12, 2000) Prior Examiner: Stephen Tu
(By Express Mail))
For: HYPOTHALAMUS-SPECIFIC) Atty. Docket No. TSRI 548.1 DIV. 1
POLYPEPTIDES)

10910 U.S. PTO
09/735138
12/12/00

STATEMENT UNDER 37 CFR 1.825

Commissioner for Patents
BOX PATENT APPLICATION
Washington, D. C. 20231

Sir:

I hereby state that, to the best of my information and belief, the content of the paper and computer readable copies of the substitute sequence listing submitted pursuant to 37 CFR 1.825, respectively, is the same.

Respectfully submitted,

OLSON & HIERL, LTD.

By Talivaldis Cepuritis
Talivaldis Cepuritis (Reg. No. 20,818)

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SCANNED, #

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Sutcliffe, J. Gregor
Gautvik, Kaare M.
De Lecea, Luis
Bloom, Floyd E.
Danielson, Patria E.
Kilduff, T.S.
Gautvik, Vigdis T.
Foye, Pamela E.

(ii) TITLE OF INVENTION: Hypothalamus-Specific Polypeptides

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Olson & Hierl, Ltd.
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(F) ZIP: 60606

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: Not yet Known (Division of 09/230,896
filed 02-FEB-1999)
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/023,220
(B) FILING DATE: 02-AUG-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Talivaldis Cepuritis
(B) REGISTRATION NUMBER: 20,818
(C) REFERENCE/DOCKET NUMBER: TSRI 548.1 DIV.1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 312-580-1180
(B) TELEFAX: 312-580-1189

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 130 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Met Asn Leu Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
1           5           10           15

Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
20           25           30

Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu
35           40           45

Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr
50           55           60

Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln
65           70           75           80

Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
85           90           95

Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr Pro Cys Pro Gly Arg
100          105          110

Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala Pro Arg Gly Gly Ser
115          120          125

Arg Val
130
```

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 130 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Asn Phe Pro Ser Thr Lys Val Pro Trp Ala Ala Val Thr Leu Leu
1           5           10           15

Leu Leu Leu Leu Leu Pro Pro Ala Leu Leu Ser Leu Gly Val Asp Ala
20           25           30
```

Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr Cys Ser Cys Arg Leu
 35 40 45
 Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile Leu Thr
 50 55 60
 Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln
 65 70 75 80
 Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
 85 90 95
 Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro His Pro Cys Ser Gly Arg
 100 105 110
 Gly Cys Pro Thr Val Thr Thr Thr Ala Leu Ala Pro Arg Gly Gly Ser
 115 120 125
 Gly Val
 130

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 569 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TAAGACGACG GCCTCAGACT CCTTGGGTAT TTGGACCACT GCACCGAAGA TACCATCTCT	60
CCGGATTACC TCTCCCTGAG CTCCAGACAC CATGAACCTT CCTTCTACAA AGGTTCCCTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCGCCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCGCAG CCTCTGCCCC ACTGCTGTCTG CCAGAAGACG TGTTCCTGCC GGCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCCGC GGGCATCCTC ACTCTGGGAA AGCGGCGACC	300
TGGACCCCCA GGCCTCCAAG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAT ATCCCTGCCC	420
TGCTCGCCGC TGTCCGACTG CAACCGCCAC CGCTTTAGCG CCCCAGGGCG GATCCAGAGT	480
CTGAACCCGT CTTCTATCCC TGTCCTAGTC CTAACCTTCC CCTCTCCTCG CCAGTCCCTA	540
GGCAATAAAG ACGTTTCTCT GTTGGTGTG	569

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TAAGACGACG GCCTCAGACT TCTTGGGTAT TTGGACCACT GCACTGAAGA GATCATCTCT	60
CCAGATTACT TTCCCCTGAG CTCCAGGCAC CATGAACTTT CCTTCTACAA AGGTTCCCTG	120
GGCCGCCGTG ACGCTGCTGC TGCTGCTACT GCTGCCACCG GCGCTGCTGT CGCTTGGGGT	180
GGACGCACAG CCTCTGCCCC ACTGCTGTCG CCAGAAGACG TGTTCCTGCC GTCTCTACGA	240
ACTGTTGCAC GGAGCTGGCA ACCACGCTGC GGGTATCCTG ACTCTGGGAA AGCGGCGGCC	300
TGGACCTCCA GGCCTCCAGG GACGGCTGCA GCGCCTCCTT CAGGCCAACG GTAACCACGC	360
AGCTGGCATC CTGACCATGG GCCGCCGCGC AGGCGCAGAG CTAGAGCCAC ATCCCTGCTC	420
TGGTCGCGGC TGTCCGACCG TAACTATCAC CGCTTTAGCA CCCCGGGGAG GGTCCGGAGT	480
TTGAACCCAT CTTCTATCCT TGTCCTGATC CAACTTCCC CCTCTGCTCG CCGCTGTCAG	540
TCTCTTGGTA AATGGCAATA AAGACGTTTC TCTGTTGGTG TG	582

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1458 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTAGGAGAC ATTGCGGCGG CGGTGGCGGC GTTGGCAGCA GCTGCAGACA TGCTGCTGCT	60
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CAAGAAACAG	ACGGAGGACA	TCAGCAGTGT	CTATGAGATC	CGGGAGAAGC	TGGGCTCGGG	120
TGCCTTCTCT	GAGGTGATGC	TGGCCCAGGA	AAGGGGCTCT	GCTCATCTTG	TGGCCCTCAA	180
GTGCATTCCC	AAGAAAGCAC	TTCGGGGCAA	GGAGGCCCTG	GTGGAGAATG	AGATCGCAGT	240
ACTCCGCAGG	ATTAGCCACC	CCAACATTGT	GGCTCTGGAG	GACGTCCACG	AGAGCCCTTC	300
CCATCTCTAC	TTGGCCATGG	AGCTGGTAAC	AGGTGGTGAA	CTGTTTGACC	GAATCATGGA	360
GCGGGGCTCC	TACACAGAGA	AGGATGCGAG	CCACCTTGTA	GGGCAGGTCC	TTGGTGCTGT	420
CTCCTACCTT	CATAGCCTGG	GCATCGTGCA	CCGGGACCTC	AAGCCTGAAA	ACCTCCTCTA	480
TGCCACACCT	TTTGAGGACT	CCAAGATCAT	GGTCTCTGAC	TTTGGCCTGT	CCAAAATTCA	540
AGCTGGCAAC	ATGCTAGGCA	CAGCCTGTGG	GACCCAGGA	TATGTGGCCC	CAGAGCTCCT	600
GGAGCAGAAA	CCCTACGGGA	AGGCCGTAGA	TGTGTGGGCC	CTGGGTGTCA	TCTCCTACAT	660
CCTGCTGTGT	GGGTACCCCC	CCTTCTATGA	TGAGAGCGAT	CCTGAACTCT	TCAGCCAGAT	720
TCTGAGGGCC	AGCTACGAGT	TTGACTCTCC	CTTTTGGGAT	GACATCTCAG	AATCAGCCAA	780
AGACTTCATT	CGGCACCTTC	TGGAACGTGA	TCCCCAGAAG	AGGTTACCT	GCCAACAGGC	840
CTTACAGCAT	CTCTGGATCT	CTGGGGATGC	AGCCTTGGAC	AGGGACATCC	TAGGTTCTGT	900
CAGTGAGCAG	ATCCAGAAGA	ATTTTGCCAG	GACCCACTGG	AAGCGTGCAT	TCAATGCCAC	960
ATCATTCCTA	CGTCACATCC	GTAAGCTGGG	ACAGAGCCCA	GAGGGTGAGG	AGGCCTCCAG	1020
GCAGGGTATG	ACCCGTCACA	GCCACCCAGG	CCTTGGGACT	AGCCAGTCTC	CCAAGTGGTG	1080
ACAACCAGGT	GGATGCCAAG	GAAGGCCAAG	TGGACTGACT	CCTAGCTTTT	CTTTCCTCCA	1140
GCCCTTTTGA	TCTCCTTCCC	TGATCCTTGT	CCCCCGGACT	GGCCTCTGTT	GGAAAGTCCA	1200
AGACCGTGGG	TGTGATGCAT	GGCACTGGGG	TATGGGGCTT	CCCAAGTATG	TCCCCAGCCT	1260
CTGTCCTTTG	TTGCTGCCAC	CCTCTATGGA	AACTGAGGAG	GTATTCAAAA	ATGGATTTGG	1320
GGGCCATCCT	TCCTGCACCT	TGCACGCACA	TATGCATTGC	GTGGCTGTTC	TGTGCTTTGC	1380
TGACTGTGGG	TGGTCCTGCT	TGTGTTGTAG	CCCTTTAGTT	CCTCCTCTTT	CCAACCAATA	1440
AAGACAAACA	GAACAATG					1458

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
1           5           10           15
Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
20           25           30
Ala Gly Ile Leu Thr Leu Gly Lys Arg Arg Pro Gly Pro Pro Gly Leu
35           40           45
Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala
50           55           60
Gly Ile Leu Thr Met Gly Arg Arg Ala Gly Ala Glu Leu Glu Pro Tyr
65           70           75           80
Pro Cys Pro Gly Arg Arg Cys Pro Thr Ala Thr Ala Thr Ala Leu Ala
85           90           95
Pro Arg Gly Gly Ser Arg Val
100
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Leu Gly Val Asp Ala Gln Pro Leu Pro Asp Cys Cys Arg Gln Lys Thr
1           5           10           15
Cys Ser Cys Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala
20           25           30
Ala Gly Ile Leu Thr Leu Gly
35
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 38 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Leu	Gly	Val	Asp	Ala	Gln	Pro	Leu	Pro	Asp	Cys	Cys	Arg	Gln	Lys	Thr
1				5					10					15	
Cys	Ser	Cys	Arg	Leu	Tyr	Glu	Leu	Leu	His	Gly	Ala	Gly	Asn	His	Ala
			20					25					30		
Ala	Gly	Ile	Leu	Thr	Leu										
			35												

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro	Gly	Pro	Pro	Gly	Leu	Gln	Gly	Arg	Leu	Gln	Arg	Leu	Leu	Gln	Ala
1				5				10						15	
Asn	Gly	Asn	His	Ala	Ala	Gly	Ile	Leu	Thr	Met	Gly				
			20					25							

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Gly Pro Pro Gly Leu Gln Gly Arg Leu Gln Arg Leu Leu Gln Ala
1 5 10 15
Asn Gly Asn His Ala Ala Gly Ile Leu Thr Met
20 25

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg Leu Tyr Glu Leu Leu His Gly Ala Gly Asn His Ala Ala Gly Ile
1 5 10 15
Leu Thr Leu Gly
20

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Arg Leu Gln Arg Leu Leu Gln Ala Asn Gly Asn His Ala Ala Gly Ile
1 5 10 15
Leu Thr Met Gly
20

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gly Asn His Ala Ala Gly Ile Leu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATGAACCTTC CTTCTACAAA GGTTCCCTGG GCCGCCGTGA CGCTGCTGCT GCTGCTACTG	60
CTGCCGCCGG CGCTGCTGTC GCTTGGGGTG GACGCGCAGC CTCTGCCCCGA CTGCTGTTCGC	120
CAGAAGACGT GTTCCTGCCG TCTCTACGAA CTGTTGCACG GAGCTGGCAA CCACGCCGCG	180
GGCATCCTCA CTCTGGGAAA GCGGCGACCT GGACCCCCAG GCCTCCAAGG ACGGCTGCAG	240
CGCCTCCTTC AGGCCAACGG TAACCACGCA GCTGGCATCC TGACCATGGG CCGCCGCGCA	300
GGCGCAGAGC TAGAGCCATA TCCCTGCCCT GGTCGCCGCT GTCCGACTGC AACCGCCACC	360
GCTTTAGCGC CCCGGGGCGG ATCCAGAGTC TGA	393

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 393 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iv) ANTI-SENSE: NO

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

[illegible]